

0570
1211

#4

OIKE

RAW SEQUENCE LISTING

DATE: 11/28/2001

PATENT APPLICATION: US/09/910,186A

TIME: 13:08:12

Input Set : A:\09910186seqlist.txt

Output Set: N:\CRF3\11212001\I910186A.raw

ENTERED

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1 <110> APPLICANT: U.S. Army Medical Research & Material Command
4 <120> TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
5   NEUROTOXIN
7 <130> FILE REFERENCE: A33626-A 067252.0107
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/910,186A
C--> 9 <141> CURRENT FILING DATE: 2001-07-20
9 <150> PRIOR APPLICATION NUMBER: PCT/US00/12890
10 <151> PRIOR FILING DATE: 2000-05-12
12 <150> PRIOR APPLICATION NUMBER: 09/611,419
13 <151> PRIOR FILING DATE: 2000-07-06
15 <150> PRIOR APPLICATION NUMBER: 60/133,865
16 <151> PRIOR FILING DATE: 1999-05-12
18 <150> PRIOR APPLICATION NUMBER: 60/133,866
19 <151> PRIOR FILING DATE: 1999-05-12
21 <150> PRIOR APPLICATION NUMBER: 60/133,867
22 <151> PRIOR FILING DATE: 1999-05-12
24 <150> PRIOR APPLICATION NUMBER: 60/133,868
25 <151> PRIOR FILING DATE: 1999-05-12
27 <150> PRIOR APPLICATION NUMBER: 60/133,869
28 <151> PRIOR FILING DATE: 1999-05-12
30 <150> PRIOR APPLICATION NUMBER: 60/133,873
31 <151> PRIOR FILING DATE: 1999-05-12
33 <150> PRIOR APPLICATION NUMBER: 08/123,975
34 <151> PRIOR FILING DATE: 1993-09-21
36 <160> NUMBER OF SEQ ID NOS: 34
38 <170> SOFTWARE: FastSEQ for Windows Version 4.0
40 <210> SEQ ID NO: 1
41 <211> LENGTH: 1332
42 <212> TYPE: DNA
43 <213> ORGANISM: Artificial Sequence
45 <220> FEATURE:
46 <223> OTHER INFORMATION: Synthetic construct based on Clostridium botulinum
47   sequence
49 <221> NAME/KEY: CDS
50 <222> LOCATION: (13)...(1326)
53 <400> SEQUENCE: 1
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56       1           5           10
58 atc atc aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg   99
59 Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu
60   15           20           25
62 atc gac ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt   147
63 Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val
64   30           35           40           45
66 aac ttc gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa   195
67 Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu

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68		50		55		60	
70	tct tcc aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct						243
71	Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser						
72		65		70		75	
74	atg tac gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac						291
75	Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr						
76		80		85		90	
78	ttc aac tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg						339
79	Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met						
80		95		100		105	
82	gaa aac aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc						387
83	Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile						
84	110		115		120		125
86	tgg act ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa						435
87	Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys						
88		130		135		140	
90	tac tct cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc						483
91	Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe						
92		145		150		155	
94	gtt acc atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac						531
95	Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn						
96		160		165		170	
98	ggc cgt ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac						579
99	Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His						
100		175		180		185	
102	gct tct aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac						627
103	Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His						
104	190		195		200		205
106	cgc tac atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac						675
107	Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn						
108		210		215		220	
110	gaa aaa gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc						723
111	Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile						
112		225		230		235	
114	ctg aaa gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac						771
115	Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr						
116		240		245		250	
118	atg ctg aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta						819
119	Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val						
120		255		260		265	
122	ggt atc cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg						867
123	Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met						
124	270		275		280		285
126	act acc aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc						915
127	Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe						
128		290		295		300	
130	atc atc aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac						963
131	Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn						
132		305		310		315	

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134 aat gat cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt 1011
135 Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg
136      320      325      330
138 ctg gct acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct 1059
139 Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala
140      335      340      345
142 ctg gaa atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa 1107
143 Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys
144 350      355      360      365
146 tcc aag aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag 1155
147 Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln
148      370      375      380
150 gac aac aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac 1203
151 Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn
152      385      390      395
154 aat atc gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa 1251
155 Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu
156      400      405      410
158 cgt tcc tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat 1299
159 Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp
160      415      420      425
162 gac ggt tgg ggt gaa cgt ccg ctg taa gaattc 1332
163 Asp Gly Trp Gly Glu Arg Pro Leu *
164 430      435
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 437
169 <212> TYPE: PRT
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: Synthetic construct based on Clostridium botulinum
174 sequence
177 <400> SEQUENCE: 2
178 Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn
179 1      5      10      15
180 Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
181      20      25      30
182 Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
183      35      40      45
184 Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
185      50      55      60
186 Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
187 65      70      75      80
188 Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
189      85      90      95
190 Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
191      100      105      110
192 Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
193      115      120      125
194 Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln

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195      130      135      140
196 Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
197 145      150      155      160
198 Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
199      165      170      175
200 Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
201      180      185      190
202 Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
203      195      200      205
204 Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
205      210      215      220
206 Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
207 225      230      235      240
208 Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
209      245      250      255
210 Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
211      260      265      270
212 Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
213      275      280      285
214 Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
215      290      295      300
216 Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
217 305      310      315      320
218 Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
219      325      330      335
220 Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
221      340      345      350
222 Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn
223      355      360      365
224 Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn
225      370      375      380
226 Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala
227 385      390      395      400
228 Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser
229      405      410      415
230 Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp
231      420      425      430
232 Gly Glu Arg Pro Leu
233      435
236 <210> SEQ ID NO: 3
237 <211> LENGTH: 1323
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Synthetic construct based on Clostridium botulinum
243      sequence
246 <221> NAME/KEY: CDS
247 <222> LOCATION: (13)...(1314)
248 <223> OTHER INFORMATION: Synthetic Construct

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250 <400> SEQUENCE: 3
251 gaattcgaaa cg atg tct acc ttc act gaa tac atc aag aac atc atc aat 51
252           Met Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn
253           1           5           10
255 acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac ctg 99
256 Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
257       15           20           25
259 tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc gat 147
260 Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
261   30           35           40           45
263 ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc aaa 195
264 Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
265           50           55           60
267 atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac gaa 243
268 Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
269           65           70           75
271 aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac tcc 291
272 Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
273       80           85           90
275 atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac aat 339
276 Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
277       95           100           105
279 tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act ctg 387
280 Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
281 110           115           120           125
283 cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct cag 435
284 Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
285           130           135           140
287 atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc atc 483
288 Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
289           145           150           155
291 acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt ctg 531
292 Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
293       160           165           170
295 atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct aat 579
296 Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
297       175           180           185
299 aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac atc 627
300 Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
301 190           195           200           205
303 tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa gaa 675
304 Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
305           210           215           220
307 atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa gac 723
308 Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
309           225           230           235
311 ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg aat 771
312 Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
313       240           245           250

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VERIFICATION SUMMARY

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Input Set : A:\09910186seqlist.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date